

75185
Delaval, Jan

From: Huynh, Phuong N.
Sent: Monday, September 09, 2002 1:11 PM
To: Delaval, Jan
Subject: RE: 09/811,367

Jan,

Please search polypeptide of SEQ ID NO: 1 against commercial and interference databases.

Thanks,
Neon
Art unit 1644
Mail 9E12
Tel 308-4844

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

A; Cross-references: GB:X54869; NID:935058; PIDN:CAA38650.1; PID:935059
 A; Experimental source: natural killer cell
 C; Genetics:
 A; Gene: GDB:KLRC1; NKG2
 A; Cross-references: GDB:138773; OMIM:161555
 A; Map position: 12pter-12qter
 C; Superfamily: natural killer cell receptor PI; C-type lectin homology
 C; Keywords: alternative splicing; glycoprotein; transmembrane protein
 F; 119-229/Domain: C-type lectin homology <C>
 F; 102,-03,151,180/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F; 119-130,147-229,208-221/Disulfide bonds: #status predicted

Query Match 18.6%; Score 190; DB 2; Length 233;
 Best Local Similarity 27.8%; Pred. No. 1.9e-10; Mismatches 86; Indels 22; Gaps 8;
 Matches 55; Conservative 35; Mismatches 86; Indels 22; Gaps 8;

QY 5 VIVSMELPLPTAQANQDYGPKQKSSK--PSC-SCLVIAITGLVIAVIL---SVLHQ 57
 Db 38 IYHAELNLQKASQ---DPQGNDRTYHCKDPLSAPEKLVIGLIGLICLILMASVTTWIP 94
 QY 58 WILCQGSNSYV-----CASCSPCPDRMKYGNHCYYSVEEKDWNSLEFLARDSHL 110
 Db 95 SLLIQRNNSLNTRQKARHCHCQPEWFTYNSCNYIGKERTWESLACTSKNSL 154
 QY 111 LVITDNDQBNMSLILQVFLFEEFCWIGL-RNNSGWNPEDGSPLNFR--LSSNSFVOTCGAIN 167
 Db 155 LSIDNEEFEMKFLSISFSS--WIGVFRNNSHHPWTMNGLAFKHEIKDSDNAELNCAVLQ 212
 QY 168 KNGLQASCSCEVPLHGCK 185
 Db 213 VNRILKSAQCGSSIIYHCK 230

RESULT 6

natural killer cell receptor group 2-C, splice form 1 - human
 Natural killer cell receptor group 2-D - human

N; Alternative names: NKG2-C
 C; Species: Homo sapiens (man)
 C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 19-May-2000
 C; Accession: PT0374

R; Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
 J. Exp. Med. 173, 1017-1020, 1991
 A; Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type II
 A; Reference number: PT0372; MUID:9118434
 A; Accession: PT0374

A; Residues: 1-231 <HOD>
 A; Cross-references: EMBL:X54869; NID:935060; PIDN:CAA38651.1; PID:935061
 A; Experimental source: natural killer cell
 C; Genetics:
 A; Gene: GDB:KLRC2; NKG2-C
 A; Cross-references: GDB:977095
 A; Map position: 12p13-12p13
 C; Superfamily: natural killer cell receptor PI; C-type lectin homology
 C; Keywords: glycoprotein; transmembrane protein
 F; 71-96/Domain: transmembrane #status predicted <TRA>
 F; 27,100,149,178/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.8%; Score 182; DB 2; Length 231;
 Best Local Similarity 27.8%; Pred. No. 1.1e-09; Mismatches 76; Indels 14; Gaps 5;
 Matches 47; Conservative 32; Mismatches 76; Indels 14; Gaps 5;

QY 24 PQQKSSSKPSCSLVATIGLTAVALSLLQWILCQGSNSY-----CASCSPCPDRW 79
 Db 67 PPEKLTAEVLGICIV----LMAVTKTIVLIPFLRQNSNPNTRQKARHCHCPEEW 121
 QY 80 MKYGNHCVYFSVEEKDWNSLEFLARDSHLWITDQEMSLQVFLSEAFCWIGL-RNN 138
 Db 122 ITYNSQSYVIGKERTTWEESLACTNSNSLSDNREIKELASLPS- WIGVRS 179

RESULT 7

natural killer cell receptor group 2-D - human
 Natural killer cell receptor group 2-D - human

N; Alternative names: integral membrane protein NKG2-D
 C; Species: Homo sapiens (man)
 C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 05-May-2000
 C; Accession: PT0375
 R; Houchins, J.P.; Yabe, T.; McSherry, C.; Bach, F.H.
 J. Exp. Med. 173, 1017-1020, 1991
 A; Title: DNA sequence analysis of NKG2, a family of related cDNA clones encoding type II
 A; Reference number: PT0372; MUID:9118434
 A; Accession: PT0375

A; Residues: 1-216 <HOU>
 A; Cross-references: EMBL:X54870; NID:935062; PIDN:CAA38652.1; PID:935063
 A; Experimental source: natural killer cell
 A; Note: Translation of nucleotide sequence is not complete
 C; Keywords: transmembrane protein

Query Match 17.6%; Score 180; DB 2; Length 216;
 Best Local Similarity 26.8%; Pred. No. 1.5e-09; Mismatches 42; Conservative 31; Mismatches 52; Indels 32; Gaps 5;

QY 37 CLVATIG-----LITAVLSSLVYQWILCQGSNSYTCASCSPCPDRMKYGNHCY 88
 Db 57 CFTAVAMGIRPITIMVIAWSAVFLNSLFNQEVQIP---LTFSYCCGPCKPNWICYRNQY 112
 QY 89 FSVEEKDWNSLEFLARDSHLWITDQEMSLQVFLSEAFCWIGL--RNSGWRWED 145
 Db 113 FDEDSKNWVYQSACOMSQNSLAKVYSKEDDL--LVSYHAWGLVHPTGNSQED 170
 QY 146 GSPINFSRI-----SSNSFVOTCGAIN 167
 Db 171 GSTLSPNLITIEMOKGDCALYASSFKGYIENCSTPN 207

RESULT 8

natural killer cell receptor group 2-C, splice form 2 - human
 Natural killer cell receptor group 2-C, splice form 2 - human

N; Alternative names: NKG2-C
 C; Species: Homo sapiens (man)
 C; Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 19-May-2000
 C; Accession: I54524
 R; Adankiewicz, T.V.; McSherry, C.; Bach, F.H.; Houchins, J.P.
 A; Title: Natural killer lectin-like receptors have divergent carboxy-termini, distinct
 A; Reference number: I54524; MUID:9102823
 A; Accession: I54524
 A; Status: Preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 1-240 <RES>
 A; Cross-references: GB:L14542; NID:9292360; PIDN:AAI16833.1; PID:9292361
 C; Genetics:
 A; Gene: GDB:KLRC2; NKG2-C
 A; Cross-references: GDB:9787095
 A; Map position: 12p13-12p13
 C; Superfamily: natural killer cell receptor PI; C-type lectin homology

Query Match 17.4%; Score 178.5; DB 2; Length 240;
 Best Local Similarity 28.6%; Pred. No. 2.4e-09; Mismatches 70; Indels 15; Gaps 6;
 Matches 46; Conservative 30; Mismatches 70; Indels 15; Gaps 6;

QY 24 PQQKSSSKPSCSLVATIGLTAVALSLLQWILCQGSNSY-----CASCSPCPDRW 79
 Db 67 PPEKLTAEVLGICIV----LMAVTKTIVLIPFLRQNSNPNTRQKARHCHCPEEW 121
 QY 80 MKYGNHCVYFSVEEKDWNSLEFLARDSHLWITDQEMSLQVFLSEAFCWIGL-RNN 138

RESULT 9

A46274

HIV gp120-binding C-type lectin - human

C;Species: Homo sapiens (man)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-1995

C;Accession: A46274

R;Curtis, B.M.; Scharnweber, S.; Watson, A.J. 1992

A;Title: Sequence and expression of a membrane-associated C-type lectin that exhibits C-type lectin activity

A;Reference number: A46274; MUID:92390446

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-404 <CUR>

A;Experimental source: placenta

A;Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIPI:113135)

C;Superfamily: C-type lectin homology <LCH>

Query Match 17.2%; score 176; DB 2; length 404; Best Local Similarity 30.7%; Pred. No. 6.9e-09; Matches 39; Conservative 23; Mismatches 53; Indels 12; Gaps 5;

QY 72 CPCCPDRMKYGNHCVYFVEEKDNNSLEFLCLARDSHLIVITQEMLLQVLESA-- 129

Db 253 CHPCPWEWTFEGNCYFMSNORNWHDSTACKEVGAQYVNIKSAEONFLOQLSRSNR 312

QY 130 FCGIGLR--NNSG-WRWEDEGPL--NFSRL---SSNSFVQTCGAINKNGLQASSCEVP 179

Db 313 FTMGLSLDUNQEGTWWQVWGDSPPLSPFKQYWNRGEPPNNGEEDCAEFSQNGWNDKCNLA 372

QY 180 LRGVKK 186

Db 373 KFWICKK 379

RESULT 10

A33917

NK-cell receptor P1 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 24-Sep-1999

C;Accession: A33917

R;Giorda, R.; Rudert, W.A.; Vavassori, C.; Chambers, W.H.; Hiserodt, J.C.; Trucco, M. 1990

A;Title: NKR-P1, a signal transduction molecule on natural killer cells.

A;Reference number: A33917; MUID:90378305

A;Accession: A33917

A;Status: preliminary

A;Molecule type: mRNA

Query Match 17.1%; score 175.5; DB 2; length 304; Best Local Similarity 27.5%; Pred. No. 7.1e-09; Matches 39; Conservative 27; Mismatches 61; Indels 15; Gaps 5;

QY 59 ITCQSNYSTGAS-GPSCPDPDRMKYGNHCVYFSVEEKDNNSLEFLCLARDSHLIVITDNO 117

Db 156 LTCQLANLKKNGSEAVCAPPHTERFGSCWVSESPSKWSEBDKVRLESHLHVYV 215

QY 118 EMSLQFVPSBACFGIGLRNNSG-WRWEDEGPL---NFSRISNSFV-----OTCG 164

Db 216 EQNFLQNLANVNSWIGLTDONGPWRWDGIDFERGFKNWPQDNWFGHGLGGEDCA 275

QY 165 AINKNG-LQASSCEVPHLGVK 185

Db 276 HITGGPWNDDVCORTFRWICE 297

RESULT 12

JH0822

Lymphocyte early activation antigen AIM/CD69 - human

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 08-Oct-1999

C;Accession: JH0822; 156167; S60753

R;Lopez-Cobrera, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez J. Exp. Med. 178, 537-547, 1993

A;Title: Molecular cloning, expression, and chromosomal localization of the human ear mitting receptors.

A;Reference number: JH0822; MUID:93340630

A;Molecule type: mRNA

A;Residues: 1-199 <COP>

A;Cross-references: GB:222576; NID:9397938; PIDN:CAA80298.1; PID:9397939

Query Match 17.2%; score 175.5; DB 2; length 223; Best Local Similarity 27.1%; Pred. No. 4.2e-09; Matches 49; Conservative 44; Mismatches 67; Indels 21; Gaps 9;

QY 24 PQOKSSSSKPSCLSCVWATIGL-TAVLISVLVQQ----WILCGGSNYSCTACPS-- 74

Db 35 PRSHRAKLSCADILVILVAVMSILVRLVWQPSVERCRVLIQ-ENLSKTS-PAKL 92

A; Note: the authors translated the codon CAA for residue 110 as Glu
 R; Hamann, J.; Fliebig, H.; Strauss, M.
 A; Title: Expression cloning of the early activation antigen CD69, a type II integral membrane protein expressed in the human early lymphocyte activation antigen
 A; Reference number: 156167; MUID:93267093
 A; Status: translated from GB/EMBL/DDBJ
 A; Molecule type: mRNA
 A; Residues: 1-199 <SAN>
 A; Cross-references: GB:107555; NID:9291897; PIDN:AAB46359_1; PID:9291898
 R; Santos, A.G.; Lopez-Cabrera, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.
 A; Title: Structure of the gene coding for the human early lymphocyte activation antigen receptors.
 A; Reference number: S60753
 A; Accession: S60753
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-199 <SAN>
 A; Cross-references: EMBL:230426; NID:9525242; PIDN:CAA83017_1; PID:9558352
 C; Comment: This protein is the earliest inducible cell surface glycoprotein expressed in C; Genetics:
 A; Gene: GDB:CD69
 A; Cross-references: GDB:132925; OMIM:107273
 A; Map Position: 12p13-12p12
 C; Superfamily: C-type lectin homology
 C; Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
 F; 39-64/Domain: transmembrane #status Predicted <TMM>
 F; 18-194/Domain: C-type lectin homology <LCH>
 F; 18-30/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status Predicted
 F; 31/Binding site: phosphate (Thr) (covalent) (by casein kinase II) (covalent) #status Predicted
 F; 166/Binding site: carbohydrate (Asn) (covalent) #status Predicted

Query Match 17.0%; Score 174; DB 2; Length 199;
 Best Local Similarity 22.9%; Pred. No. 5.2e-09;
 Matches 40; Conservative 33; Mismatches 76; Indels 26; Gaps 5;

QY 30 SSKPSCSCLVAITLGLITAVLVLVSLVLYKWLQCGNSNTSCASC-----SC 75
 Db 30 STRHEGSFQVPLCAVMVNVFTILILIALSLSVQY----NCPGQTFSMPSDSHVSSC 85
 QY 76 PDRWKYGNHCVYFSVKEWDWSSLERCLARDSHLWITDNOEMSLLQVLFSEAFCWIGL 135
 Db 86 SEDWVGYORKCVFISTVKRSWMSAONACSEHQATLAVIDSEKDNFEEKRYAGREEHWGL 145

QY 136 RNNSG-WRWEQGSPLN-FSRISNSNFVQTAGAINKNGLQASSCEVPLHGVCK 186
 Db 146 KKEPGHFWKWSNGKEFNFWFNTVGSDK---CVFLKNTEVSSMCECKNLWICNK 196

RESULT 13

QY 27 KSSSKPKSCLVAVI---TGLITAVL-----SYLIV----- 56
 Db 92 KETFSNFSSSTLMEFGALDTLGSTNAILTSWAQLEERQOQLKADHSTLFLKHFPMD 151

QY 57 -QWILCQ---GSWYSTCASCSPCPDRMMKYGNCIYVFSEKWNSSLEFCCLARDSHL 111
 Db 152 LRTLTCOLAYFOQNGTEC----CPVNWFGGSCWYFGRGSDGSLRWTAEAOYQCOLENAHLL 206

QY 112 VITDNOEMSLLQVFLSEAFCWIGLURNNSG-WRWEQGSPLNFSRISNSIV----- 161
 Db 207 VINSREEQDFVYKRSQHFIWIGLTDROGSMWKWDGTDYR-SNYRNWAFTOPDNWQHGEO 265

QY 162 ---TCGAINKG-LQASSCEVPLHGVCKVR 188
 Db 266 GGEDCAEILSDGHWNDFCQOQVNRWCKRR 297

Query Match 16.5%; Score 169; DB 2; Length 237;
 Best Local Similarity 21.6%; Pred. No. 1.8e-08;
 Matches 52; Conservative 39; Mismatches 92; Indels 58; Gaps 9;

RESULT 14

QY 88 YFSVTEKDNSSLEPCLARDSHLWITDNOEMSLLQVLFSEAFCWIGLNNNSG---WRW 143
 Db 119 FISTESASASHQDSEKDCARMBAHLLVINTQEQDIFQNLQEESEAYFVGLSDPEGRHWQ 178

QY 144 EDGGLPLNFRNRSISF-----VQTCGAIN-----KNGLQASSECEVPLHGVCKVR 188
 Db 179 VDQTPYN---ESSTFWHPPREPSPDPNERNRCVVLNFRKSPKRKGWNVDVNCLGPORSVCEMMK 234

QY 189 L 189

Db 235 I 235

RESULT 15

QY 1 MTDWSVYIYSMEL-----PPATOANDYGGQKSSSSKPSOCLVAVITGLUTAVL 50
 Db 1 MTSELTYAEVRFKNBFKSSGINTASSAASKERTAPLKNNGFPKLUCLASLILFFLLAIS 60

QY 51 LSV-----LIQWICLQGSY---STCASCOPSPDRMKYGNHCV 87

Db 61 FFLFREVIFQKSYOLLEKTKTKEVHTTLECYKVNMPVETAWSC---CPENWKSPSSNCY 118

QY 88 YFSVTEKDNSSLEPCLARDSHLWITDNOEMSLLQVLFSEAFCWIGLNNNSG---WRW 143
 Db 119 FISTESASASHQDSEKDCARMBAHLLVINTQEQDIFQNLQEESEAYFVGLSDPEGRHWQ 178

QY 144 EDGGLPLNFRNRSISF-----VQTCGAIN-----KNGLQASSECEVPLHGVCKVR 188
 Db 179 VDQTPYN---ESSTFWHPPREPSPDPNERNRCVVLNFRKSPKRKGWNVDVNCLGPORSVCEMMK 234

QY 189 L 189

Db 235 I 235

Query Match 16.3%; Score 167; DB 2; Length 301;
 Best Local Similarity 25.9%; Pred. No. 3.6e-08;
 Matches 55; Conservative 29; Mismatches 72; Indels 56; Gaps 9;

QY 27 KSSSKPKSCLVAVI---TGLITAVL-----SYLIV----- 56
 Db 92 KETFSNFSSSTLMEFGALDTLGSTNAILTSWAQLEERQOQLKADHSTLFLKHFPMD 151

QY 57 -QWILCQ---GSWYSTCASCSPCPDRMMKYGNCIYVFSEKWNSSLEFCCLARDSHL 111
 Db 152 LRTLTCOLAYFOQNGTEC----CPVNWFGGSCWYFGRGSDGSLRWTAEAOYQCOLENAHLL 206

QY 112 VITDNOEMSLLQVFLSEAFCWIGLURNNSG-WRWEQGSPLNFSRISNSIV----- 161
 Db 207 VINSREEQDFVYKRSQHFIWIGLTDROGSMWKWDGTDYR-SNYRNWAFTOPDNWQHGEO 265

QY 162 ---TCGAINKG-LQASSCEVPLHGVCKVR 188
 Db 266 GGEDCAEILSDGHWNDFCQOQVNRWCKRR 297

Query Match 16.5%; Score 169; DB 2; Length 237;
 Best Local Similarity 21.6%; Pred. No. 1.8e-08;
 Matches 52; Conservative 39; Mismatches 92; Indels 58; Gaps 9;

RESULT 15

T28141

C type lectin, B locus - chicken

C;Species: Gallus gallus (chicken)

C;Accession: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T28141

R;Mine, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility complex
A;Reference number: 220475
A;Accession: T28141
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-156 <MIL>
A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAA18961.1
A;Experimental source: clone CB12
C;Genetics:
A;Gene: BlcC
A;Map position: 16
A;Introns: 17/1; 74/3; 110/2

Search completed: September 9, 2002, 15:00:27
Job time: 341 sec

FT	DISULFID	152	165	BY SIMILARITY.
FT	CARBOHYD	83	83	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	132	132	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	179	AA;	1884D99E8D9588A7 CRC64;
DR	SHART, SM00034; CLECT; 1;			
DR	PROSITE; PS000615; C-TYPE LECTIN_1; FALSE_NEG.			
DR	PROSITE; PS00041; C-TYPE LECTIN_2; 1.			
KW	Antigen; B-cell; Glycoprotein; Transmembrane; Lectin; Signal-anchor;			
KW	Phosphorylation.			
FT	DOMAIN	1	40	CYTOSPLASMIC (POTENTIAL).
FT	TRANSMEM	41	61	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN (POTENTIAL)).
FT	DOMAIN	62	199	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	67	199	C-TYPE LECTIN (LONG FORM).
FT	DISULFID	68	185	BY SIMILARITY.
FT	DISULFID	96	194	BY SIMILARITY.
FT	DISULFID	173	186	BY SIMILARITY.
FT	CARBOHYD	150	150	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	166	166	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	199	AA;	39F8E4941D36D4F6 CRC64;
Query Match		19.2%		Score 196.5; DB 1; Length 179;
Best Local Similarity		32.7%		Pred. No. 9.9e-12; Pred. No. 9.9e-12; Indels 15; Gaps 7;
Matches		53;		Conservative 25; Mismatches 69; Indels 15; Gaps 7;
Qy	35	CSCLVATLGLITAVLISVLVWILCGGSN-YSTCASCPCDRWMKGNHCVYFSE	92	
Qy	93	EKDWNSSLEFLCLARDSHLWITDNOEMSLQVFSEAFCWIGL--RNNSGWRWEDGSP	149	
Db	20	CISLMA-TLGILKLNSTKLSIPEAFTGCPNIELQKDSDCCSCEKWKYRCNCYFISE	78	
Db	79	OKTWNESRHLCASQKSSLQQLQNTDEDFMS--SSQOFWIGLSEEHITAWLWENGSA	136	
Qy	150	NFSRISNSF---VQTCGAINKG-LOASSEVPLHGCKK	186	
Db	137	--SOYLFPSFENTKNCIAYNNGNALEDESCDKNRYICKQ	176	
RESULT	2			
CD69_MOUSE				
ID	C69_MOUSE			STANDARD; PRT: 199 AA.
AC	P37217;			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	01-OCT-1994 (Rel. 30, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Early activation antigen C69.			
GN	C69.			
OS	Mus musculus (Mouse).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.			
OC	NCBI_TAXID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93314711; Pubmed=8100776;			
RA	Ziegler S.F., Ransdell F., Hjerrild K.A., Armitage R.J.,			
RA	Grabshtain K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,			
RA	Alderson M.R.;			
RT	"Molecular characterization of the early activation antigen CD69: a type II membrane glycoprotein related to a family of natural killer cell activation antigens."			
RT	Bur. J. Immunol. 23:1643-1648(1993).			
RL				
CC	- SIGNAL TRANSMITTING RECEPTOR IN LYMPHOCYTES, NATURAL KILLER (NK) CELLS, AND PLATELETS.			
CC	- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.			
CC	- SUBCELLULAR LOCATION: TYPE II membrane protein.			
CC	- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T CELLS, B-CELLS, NATURAL KILLER CELLS, NEUTROPHILS AND PLATELETS.			
CC	- DEVELOPMENTAL STAGE: EARLIEST INDUCIBLE CELL SURFACE GLYCOPROTEIN ACQUIRED DURING LYMPHOID ACTIVATION.			
CC	- INDUCTION: BY THE ACTIVATION OF T LYMPHOCYTES			
CC	- PTM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BOTH MATURE T-CELLS AND ACTIVATED T LYMPHOCYTES (BY SIMILARITY).			
CC	- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; L23638; ; NOT_ANNOTATED_CDS.			
DR	HSSP; P05451; ILIT.			
DR	MGB; MGI:88243; Cdg69.			
DR	INTERPRO; IPR01304; lectin_c.			
DR	PFam; PF00059; Lectin_c; 1.			
RESULT	3			
NK1_MOUSE				
ID	NK1_MOUSE			STANDARD; PRT: 227 AA.
AC	P27811;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Natural killer cell surface Protein P1-2 (NKR-P1 2) (NKR-P1.7).			
GN	LY55A OR LY55.			
OS	Mus musculus (Mouse).			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TAXID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91349596; Pubmed=1890421;			
RA	Giorda R., Trucco M.,			
RA	"Mouse NKR-P1. A family of genes selectively coexpressed in adherent lymphokine-activated killer cells."			
RA	J. Immunol. 147:1701-1708(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9203158; Pubmed=1680927;			
RA	Yokoyama W.M., Ryan J.C., Hunter J.J., Smith H.R.C., Stark M., Seaman W.E.,			
RA	"Mouse NKR-P1 and genetic linkage with LY-49. cDNA cloning of mouse NKR-P1 and genetic linkage with LY-49. Identification of a natural killer cell gene complex on mouse chromosome 6."			
RA	J. Immunol. 147:3229-3236(1991).			
CC	- FUNCTION: MAY FUNCTION AS SIGNAL-TRANSMITTING RECEPTOR.			
CC	- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.			
CC	- SUBCELLULAR LOCATION: TYPE II membrane protein.			
CC	- TISSUE SPECIFICITY: NATURAL KILLER CELLS.			

CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
 CC
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 CC
 DR EMBL; M77676; AAA39822.1; -.
 DR MGD; MGI:107540; LY55A.
 DR InterPro; IPR001304; lectin_c.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 KW GLYCOPROTEIN; Antigen; Transmembrane; Signal-anchor; Lectin.
 FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 FT DOMAIN 63 227 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 94 105 BY SIMILARITY.
 FT DISULFID 122 210 BY SIMILARITY.
 FT DISULFID 189 202 BY SIMILARITY.
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 39 39 S -> L (IN REF. 2).
 SQ SEQUENCE 227 AA; 25689 MW; 0599a2587DF0B615 CRC64;

Query Match 18.7%; Score 191; DB 1; Length 227;
 Best Local Similarity 27.4%; Pred. No. 4.2e-11;
 Matches 49; Conservative 43; Mismatches 71; Indels 16; Gaps 7; .

QY 24 PQQKSSSKPSCSCIVAVITGLL-TAVLLSVLYQ---WILCGGS-NYST-CASCPS 74
 Db 34 PRSHRSALKLSCAGLILLVTLIGKSVLVRVLIOPSIERKCYVILQBNLKNTDOSAKL 93
 QY 75 CPDRMKYGHCVTYSVEEKDWNSLIECLARDSHLVLITDQENASLQLQVLFSEAF-CW 132
 Db 94 CPQDWLSHRKCFHVQSNTWEEGLVDCDGKATMLQDEELRFLPLDSIKEKYNFW 153
 QY 133 IGLR---ANSGWRWEDGSPNFS--RISSNSFVQTCGAINKNGLOASCEVPLHGVCKK 186
 Db 154 IGLRTYLPDNWKWINGSTLNSDVLKITGTDENDSCAISGDKVYFESCNSDNRWICQK 212

RESULT 4
 NKGA_HUMAN STANDARD; PRT; 233 AA.
 ID NKGA_HUMAN
 AC P26715;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DE NKG2A/NKG2-B type II integral membrane protein (NKG2-A/B activating
 NK receptor)
 GN KLRCL OR NKG2A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
 OC NCBI_TaxId=9606;
 RN SEQUENCE FROM N.A.
 RX MEDLINE-31178334; PubMed=2007850;
 RA Houchins J.P., Yabe T., McShea C., Bach F.H.;
 RT "DNA sequence analysis of NKG2, a family of related cDNA clones
 RT encoding type II integral membrane proteins on human natural killer
 RT cells.";
 J. Exp. Med. 173:1017-1020(1991).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96337918; PubMed=8753859;
 RA Plougastel B.; Jones T.; Trowsdale J.;
 CC "Genomic structure, chromosome location, and alternative splicing of
 the human NKG2A gene";
 RL Immunogenetics 44:286-291(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-98260668; PubMed=9598306;
 RA Plougastel B.; Trowsdale J.;
 RT "Sequence analysis of a 62-kb region overlapping the human KLRC
 RT cluster of genes";
 RL Genomics 49:193-199(1998).
 CC -!- FUNCTION PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC
 CC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
 CC -!- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERO-DIMER WITH CD94.
 CC -!- ALTERNATIVE SPlicing PRODUCTS: THE NKG2-A AND -B PEPTIDES APPEAR TO BE
 CC -!- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
 CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; X54867; CAA38649.1; -.
 DR EMBL; X54868; CAA38650.1; -.
 DR EMBL; U5785; ARB17133.1; -.
 DR EMBL; U54783; ARB17133.1; JOINED.
 DR EMBL; U54784; ARB17133.1; JOINED.
 DR EMBL; U54785; ARB17133.1; JOINED.
 DR EMBL; AF023840; AAC11488.1; -.
 DR PIR; PT0372; PT0372.
 DR PIR; PT0373; PT0373.
 DR HSSP; PI658; 15SLL.
 DR MIM: 161555; -.
 DR InterPro; IPR001304; lectin_c.
 DR Pfam; PF00059; lectin_c; 1.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
 DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
 KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
 KW Glycoprotein; Alternative splicing.
 FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 FT DOMAIN 94 233 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 71 93 C-TYPE LECTIN (LONG FORM).
 FT DOMAIN 118 231 BY SIMILARITY.
 FT DISULFID 119 130 BY SIMILARITY.
 FT DISULFID 147 229 BY SIMILARITY.
 FT DISULFID 208 221 BY SIMILARITY.
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPLIC 96 113 MISSING (IN ISOFORM NKG2-B).
 SQ SEQUENCE 233 AA; 26287 MW; 1654BD7958C81A84 CRC64;

Query Match 18.6%; Score 190; DB 1; Length 233;
 Best Local Similarity 27.8%; Pred. No. 5.4e-11;
 Matches 55; Conservative 35; Mismatches 86; Indels 22; Gaps 8;

QY 5 VVYSMELPPTAQOQNDYQPOQKSSSK--PSCC-SOLVATLGLLTAVL---SVLYQ 57
 Db 38 ITYAEINLQRASQ--DFQGNDKTYICKDPLPSAEPKLVIGLIGLILMASWVTVIP 94

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CC

DR EMBL: X54870; CAA38652.1; -.

DR EMBL: AJ001687; CAA04925.1; -.

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CC

DR MIM: 602833; -.

DR Interpro: IPR001304; lectin_c.

DR Pfam: PF00059; lectin_c; 1.

DR SMART: SM00034; CLECT; 1.

DR PROSITE: PS00615; C_TYPELECTIN_1; FALSE_NEG.

DR PROSITE: PS0041; C_TYPELECTIN_2; 1.

KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin; Glycoprotein.

FT DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 52 72 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

FT DOMAIN 98 216 EXTRACELLULAR (POTENTIAL).

FT DISULFID 99 213 C-TYPE LECTIN (LONG FORM).

FT DISULFID 127 211 BY SIMILARITY.

FT DISULFID 189 203 BY SIMILARITY.

FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 216 AA: 25274 MW; C22F6BD53D7800E CRC64; SEQUENCE

Query Match 17.6%; Score 180; DB 1; Length 216;

Best Local Similarity 26.8%; Pred. No. 4 4e-10;

Matches 42; Conservative 31; Mismatches 52; Indels 32; Gaps 5;

QY 37 CLVATLGL-----LITAVLVLVLYQWILCQGSNYSTASCSPCPDRMKYGHHCY 88

Db 57 CFIAVPMGIRPLIMVIAVLSAVFLNSLNPQEQVQI---LTESYCGCPCKPNWCKNQYQ 112

QY 89 FSVKEKWDNSLFLARDLSSLLVTDNQEMSLQVFLSEAFCWIGL--RNNSGRWED 145

Db 113 FFDESKWYBQSACNSQNALVSKYVSKEDDILK--LVKSYHWMGLVHPTNGSQWQED 170

QY 146 GSPLNFSR-----SSNSFWVOTCGATN 167

Db 171 GSILSPNLITIEMOKGDALYASSEFGYIENCSTPP 207

RESULT 7

ID NKG_E_HUMAN STANDARD; PRT; 240 AA.

NRGE_HUMAN

AC 007444; 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE NKG2-E type II integral membrane protein (NKG2-D activating NK receptor)

DE receptor)

GN KIRC3 OR NKG2E.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarhini; Hominoidea; Homo.

NCBI_TaxID:9606; [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=941102823; PubMed=8276468;

RA Adamekiewicz T.V.; Mosherry C.; Bach F.H.; Houchins J.P.;

RT "Natural killer lectin-like receptors have divergent carboxy-termini, distinct from C-type lectins." Immunogenetics 39:218-218(1994). [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98350122; PubMed=9693661;

RA Glienke J.; Sobolov Y.; Bröstjan C.; Steffens C.; Nguyen C.;

RA Leinrach H.; Hofer E.; Francis F.;

RT "The genomic organization of NKG2C, E, F, and D receptor genes in the human killer gene complex." Immunogenetics 48:163-173(1998).

CC FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC CLASS I HLA-MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.

CC SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.

CC SUBCELLULAR LOCATION: Type II membrane protein.

CC TISSUE SPECIFICITY: NATURAL KILLER CELLS.

CC SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

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CC

DR EMBL: L14542; AAC16833.1; -.

DR MIM: 602892; -.

DR Interpro: IPR001304; lectin_c.

DR Pfam: PF00059; lectin_c; 1.

DR SMART: SM00034; CLECT; 1.

DR PROSITE: PS00615; C_TYPELECTIN_1; FALSE_NEG.

DR PROSITE: PS0041; C_TYPELECTIN_2; 1.

KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin; Glycoprotein.

FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

FT DOMAIN 94 240 EXTRACELLULAR (POTENTIAL).

FT DISULFID 116 230 C-TYPE LECTIN (LONG FORM).

FT DISULFID 117 128 BY SIMILARITY.

FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SEQUENCE 240 AA: 27012 MW; 20691FB21274D8A6 CRC64;

Query Match 17.4%; Score 178.5; DB 1; Length 240;

Best Local Similarity 28.6%; Pred. No. 6.9e-10;

Matches 46; Conservative 30; Mismatches 70; Indels 15; Gaps 6;

QY 24 PQQKSSSSKPSCSCLIVATLGLIATLVLVLYQWILCQGSNYST---CASCSPCPDRW 79

Db 67 PPKPLIAEVLGICIV---LMATVKEVTLIPPLEQNNSPNRTOKAPCPGHCPEW 121

QY 80 MXGNHAYYFSEEEKWDNSLFLARDLSSLLVTDNQEMSLQVFLSEAFCWIGL-RN 137

Db 122 ITVNSNCVYIGKERTWESLQACASKNSSLISIDNEEMFLASLIPSS-WIGVFRN 179

QY 138 NSGRWEDGSPNPNSR--ISSISFWVOTCGAINNGLQASSC 176

Db 180 SSIHPWVITNGAFKHEKDSHQAERNCAMLVYRGLISDC 220

RESULT 8

ID NK13_RAT STANDARD; PRT; 223 AA.

NCBI_TaxID:9613_RAT

AC P27471; 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DE Natural killer cell surface protein p1-3.2.3 (NKR-P1 3.2.3) (Antigen 3.2.3).

OS Rattus norvegicus (Rat);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.
 OX NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90378305; PubMed=23099464;
 RA Gloroda R., Roder W.A., Vassorsori C., Chambers W.H., Hiserodt J.C., Trucco M.,
 "NKR-P1, a signal transduction molecule on natural killer cells.",
 Science 249:1298-1300(1990).
 RT -I- FUNCTION: MEDIATES TRANSMEMBRANE SIGNALING IN NATURAL KILLER
 (NKR) CELLS AND SO MAY ACT AS A RECEPTOR ABLE TO SELECTIVELY
 TRIGGER NK CELL ACTIVITY.
 CC -I- SUBUNIT: HOMODIMER.
 CC -I- SUBCELLULAR LOCATION: TYPE II membrane protein.
 CC -I- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
 CC -I- MISCELLANEOUS: LIGAND BINDING MAY BE CALCIUM DEPENDENT.
 CC -I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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 or send an email to license@isb-sib.ch).
 EMBL; M62891; A35917; A35917;
 InterPro; IPR001304; lectin_c.
 DR PROSITE; PS00059; lectin_c.
 DR SMART; SM00034; CLECT; 1.
 DR PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
 KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.
 FT DOMAIN 1 43 SIGNAL-ANCHOR (TYPE-II) MEMBRANE PROTEIN
 FT TRANSMEM 44 63 (POTENTIAL).
 FT DOMAIN 64 223 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).
 FT DISULFID 94 105 BY SIMILARITY.
 FT DISULFID 122 210 BY SIMILARITY.
 FT DISULFID 189 202 BY SIMILARITY.
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 223 AA; 24551 MW; FCD12B212DDF4330 CRC64;

Query Match 17.2%; Score 175.5; DB 1; Length 223;
 Best Local Similarity 27.1%; Pred. No. 1.2e-09;
 Matches 49; Conservative 44; Mismatches 67; Indels 21; Gaps 9;

QY 24 PQQKSSSKPSCSCLVLTGGL-TAVILSVLHQ---WILCGSSNYSTCASCPS- 74
 DB 35 PRSHRLALKLSCAGLILVLVLMGVMSLVLVRLVQKPSVPCRYLQ-ENLSKTGS-PAKL 92
 QY 75 -CPDRWMMYGNIGYVFSTEKKWNSLLEFLCLARDSHLVLITDQEMSLQVF--LSEAF 130
 DB 93 KCPKDWLSHRDKCFHVSOTSIWKESELADCGGKGATLIVDQEEFLRFLRNLTRKISSF 152
 QY 131 CWIGLR--NNNSWRWEDGSPLNFS--RISNSFVQFTGAINNGLQASSCSPVPLHGVCK 185
 DB 153 -WIGLSYTLSDENWKWINGSTINSDVLSITGTEKDSCASVSDKVSESCSDNINWVQ 211
 QY 186 K 186
 DB 212 K 212

Query Match 17.1%; Score 174.5; DB 1; Length 304;
 Best Local Similarity 27.5%; Pred. No. 2.1e-09;
 Matches 39; Conservative 27; Mismatches 61; Indels 15; Gaps 5;

RESULT 9
 MGL_MOUSE
 ID MGL_MOUSE
 AC P49300;

QY 59 ILCGGSNYSTCASCPSRDRWMMYGNIGYVFSTEKKWNSLLEFLCLARDSHLVLITDQ 117
 DB 156 LTCOLANLNKNGSEVACCPHLWTERGSCYWFSESEKSWPEADKICRLENHLVWNSL 215

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CC

DR EMBL; X54870; CAA38652.1; -.

DR EMBL; AJ001687; CAA05925.1; -.

DR EMBL; AJ001688; CAA05925.1; JOINED.

DR PIR; PT0375; PT0375.

DR PIR; S19110; S19110.

DR MIM; 602893; -.

DR Interpro; IPR001304; lectin_c.

DR Pfam; PF00059; lectin_c; 1.

DR SMART; SM0034; CLEC1; 1.

DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.

DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin; Glycoprotein.

FT DOMAIN 1 51 SIGNAL_ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT TRANSMEM 52 72 (POTENTIAL).

FT DOMAIN 73 216 CTOPLASMIC (POTENTIAL).

FT DOMAIN 98 213 EXTRACELLULAR (POTENTIAL).

FT DISULFID 99 110 C-TYPE LECTIN (LONG FORM).

FT DISULFID 127 211 BY SIMILARITY.

FT DISULFID 189 203 BY SIMILARITY.

FT CARBOHYD 131 163 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 216 AA; 25274 MW; C22F6B5D33D7800E CRC64; SQ SEQUENCE

Query Match 17.6%; Score 180; DB 1; Length 216;

Best Local Similarity 26.8%; Pred. No. 4.4e-10;

Matches 42; Conservative 31; Mismatches 52; Indels 32; Gaps 5;

Qy 37 CLVATITLG-----LLTAVLISVLVLYQWILCOGSNSYSTASCSCPSCPDRWKGYHICYY 88

Db 57 CFIAVANGIRFIMVAVISVAVFLNSLNFNQEVOIP---LTESYCGCOPCKPNWICYKNNCYQ 112

Qy 89 FSVEEEDWNSSLEFCARDSHLVLITDNOEMSLLQVPLSEAFCWIGL--RNSGARWED 145

Db 113 FFDESKHWWYEQASCHMSONASILKVKYSKEDDLK--LVKSYHWMGLVHPIPTNGSWOED 170

Qy 146 GSPLNNSR-----SSNSFVQTCGAIN 167

Db 171 GSILSPNLTLTIEMQGDCALYASSFKGYIENCSTPN 207

RESULT 7

NKGE_HUMAN STANDARD; PRT; 240 AA.

AC 007444; -.

DT 01-NOV-1997 (Rel. 35. Created)

DT 01-NOV-1997 (Rel. 35. Last sequence update)

DT 01-MAR-2002 (Rel. 41. Last annotation update)

DE NKG2-E type II integral membrane protein (NKG2-D activating NK receptor)

DE KLRC3 OR NKG2E.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX NCBI_TaxId=9606;

RN [1] SEQUENCE FROM N_A.

RN MEDLINE-94102823; PubMed=8276468;

RN Adamkiewicz T.V.; McSherry C.; Bach F.H.; Houchins J.P.;

RN "Natural killer lectin-like receptors have divergent carboxy-termini, distinct from C-type lectins." Immunogenetics 39:218-218(1994). [2]

RP SEQUENCE FROM N_A.

RX MEDLINE-98350122; PubMed=9683661;

RA Glennie J.; Sobanay Y.; Brosjan C.; Steffens C.; Nguyen C., Lehbrach H.; Hofer E.; Francis F.;

RA "The genomic organization of NKG2C, E, F, and D receptor genes in the human natural killer gene complex." Immunogenetics 48:163-173(1998).

RL CLASS I HLA-MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.

CC -!- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERO-DIMER WITH CD94.

CC -!- SUBCELLULAR LOCATION: TYPE II membrane protein.

CC -!- TISSUE SPECIFICITY: NATURAL KILLER CELLS.

CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

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CC

DR EMBL; LI4542; AAA16833.1; -.

DR MIM; 602892; -.

DR Interpro; IPR001304; lectin_c.

DR Pfam; PF00059; lectin_c; 1.

DR SMART; SM0034; CLEC1; 1.

DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.

DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin; Glycoprotein.

FT DOMAIN 1 70 CTOPLASMIC (POTENTIAL).

FT TRANSMEM 71 93 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 94 240 CTOPLASMIC (POTENTIAL).

FT DOMAIN 116 230 EXTRACELLULAR (POTENTIAL).

FT DISULFID 117 128 C-TYPE LECTIN (LONG FORM).

FT DISULFID 207 220 BY SIMILARITY.

FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SEQUENCE 240 AA; 27012 MW; 20691FB21274D8A6 CRC64;

Query Match 17.4%; Score 178.5; DB 1; Length 240;

Best Local Similarity 28.6%; Pred. No. 6.9e-10;

Matches 46; Conservative 30; Mismatches 70; Indels 15; Gaps 6;

Qy 24 PQQKSSSSKPSKSCSLVATITLG-----LLTAVLISVLVLYQWILCOGSNSYST---CASCSCPDRW 79

Db 67 PEPLKTAEVLGICIV-----LMATVLKTVLIPPLEQNNSNSPNTQKARPQCHCPEW 121

Qy 80 MKYGNHCHYFYSVKEKRDWNSLLEFCARDSHLVLITDNOEMSLIQLVSEAFCWIGL-RN 137

Db 122 ITVNSNCYIGKERRTWEESLQACASKNSLISIDNEBEMKFLASILPSS--WIGVFRN 179

Qy 138 NSGRWREGSPLNFSR--ISSNSFVQTCGAINRNGLQASC 176

Db 180 SSSHPWVITNGLAFKHEIKDSRARNCAMLHYRGLSDOC 220

RESULT 8

NK13_RAT STANDARD; PRT; 223 AA.

ID NK13_RAT

AC P27471; -.

DT 01-AUG-1992 (Rel. 23, created)

DT 01-AUG-1992 (Rel. 23, last sequence update)

DT 01-JUN-1994 (Rel. 29, last annotation update)

DE Natural killer cell surface protein P1-3.2.3 (NKR-P1 3.2.3) (Antigen 3.2.3).

DE Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RESULT	13	203	COLENSNLVWVNSLRAEQNFQIOTHMSGWVWIGLTDQNGPWRWDGT	248
MGL_RAT				
ID	MGL_RAT	STANDARD;	PRT;	306 AA.
AC	P49301;			
DT	01-FEB-1996 (Rel. 33, last sequence update)			
DT	01-FEB-1996 (Rel. 33, last annotation update)			
DE	Macrophage asialoglycoprotein-binding protein (M-ASGP-BP) (Macrophage galactose/N-acetylgalactosamine-specific lectin) (MMGL).			
DE	Rattus norvegicus (Rat); Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OC	NCBI_TAXID=10116;			
OX	RN			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE=9029378; PubMed=2358462;			
RA	II M., Kurata H., Itoh N., Yamashina T., Kawasaki T.; "Molecular cloning and sequence analysis of cDNA encoding the macrophage lectin specific for galactose and N-acetylgalactosamine.", J. BIOL. CHEM. 265:11295-11298 (1990).			
RP	PRELIMINARY SEQUENCE OF 9-28.			
RX	MEDLINE=88339956; PubMed=3421964;			
RA	II M., Kawasaki T., Yamashina T.; "Structural similarity between the macrophage lectin specific for galactose/N-acetylgalactosamine and the hepatic asialoglycoprotein binding protein.", Biochem. Biophys. Res. Commun. 155:720-725 (1988).			
CC	-!- FUNCTION: RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGLACTOSAMINE UNITS.			
CC	-!- SUBUNIT: HOMO-OLIGOMER.			
CC	-!- SUBCELLULAR LOCATION: "Type II membrane protein.			
CC	-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sb-sib.ch).			
CC	-!- HOMOLOGUE: EMBL: J05495; AAA41216.1; -.			
DR	DR: P06734; IKB.			
DR	DR: InterPro: IPR01304; lectin_c.			
DR	DR: Pfam: PF00059; lectin_c; 1.			
DR	DR: SMART: SM00034; CLECT; 1.			
DR	DR: PROSITE: PS00615; C_TYPE-LECTIN_1; 1.			
DR	DR: PROSITE: PS00401; C_TYPE-LECTIN_2; 1.			
DR	DR: PROSITE: PS00615; C_TYPE-LECTIN_1; 1.			
FT	FT: DOMAIN 59 305			
FT	FT: DOMAIN 174 300			
FT	FT: DOMAIN 175 186			
FT	FT: DOMAIN 203 298			
FT	FT: DOMAIN 276 290			
FT	FT: CARBOHYD 168 168			
FT	FT: SEQUENCE 306 AA: 34242 MW: D68A5DF0B9EBF13 CRC64;			
DR	DR: InterPro: IPR01304; lectin_c.			
DR	DR: Pfam: PF00059; lectin_c; 1.			
DR	DR: SMART: SM00034; CLECT; 1.			
DR	DR: PROSITE: PS00615; C_TYPE-LECTIN_1; 1.			
DR	DR: PROSITE: PS00401; C_TYPE-LECTIN_2; 1.			
DR	DR: Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane; Calcium; Signal-anchor; Phosphorylation.			
FT	FT: INITI_MET 0 0			
FT	FT: DOMAIN 1 38			
FT	FT: TRANSMEM 39 59			
FT	FT: DOMAIN 60 283			
DR	DR: MGL_RAT			
DR	DR: InterPro: IPR01304; lectin_c.			
DR	DR: Pfam: PF00059; lectin_c; 1.			
DR	DR: SMART: SM00034; CLECT; 1.			
DR	DR: PROSITE: PS00615; C_TYPE-LECTIN_1; 1.			
DR	DR: PROSITE: PS00401; C_TYPE-LECTIN_2; 1.			
DR	DR: Lectin; Glycoprotein; Receptor; Endocytosis; Transmembrane; Calcium; Signal-anchor; Phosphorylation.			
FT	FT: DOMAIN 0 0			
FT	FT: DOMAIN 1 38			
FT	FT: TRANSMEM 39 59			
FT	FT: DOMAIN 60 283			
DR	DR: Query Match 16.1%; Score 164.5; DB 1; Length 306; Best Local Similarity 32.1%; Pred. No 1.9e-08; Matches 34; Conservative 18; Mismatches 41; Indels 13; Gaps 3; Oy 43 LGLTAVLISVLYQWICQGSNYSTCASCPSGPDRWMKGNHCVYFSKEEKDWNSLLEF 102 155 IKTLCQLAST-----KRNGSAYAC---CPLHWMHEGSCWFSQSKPPEADKY 202 103 CLARDSHLVLVTNDQEMSLLQLQFLSEAFCWIGLNRNSG-WRWEWDGS 147			

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 9, 2002, 14:41:21 ; search time 13.1 Seconds
(without alignments)
352.400 Million cell updates/sec

Title: US-09-811-367B-1
Perfect score: 1023
Sequence: MTDSVYIYMLELPTATAQN.....GLQASSCEVPLHGVCVKVRL 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : issued_Patents_AA:*

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2: /cen2_6/podata/2/1aa/5B..COMB.pep:*

3: /cen2_6/podata/2/1aa/6A..COMB.pep:*

4: /cen2_6/podata/2/1aa/6B..COMB.pep:*

5: /cen2_6/podata/2/1aa/9CTRS..COMB.pep:*

6: /cen2_6/podata/2/1aa/backfile1.pep:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	% Match	Length	DB ID	Description
1	525.5	51.4	188	3	US-08-722-126A-5	Sequence 5, Appli
2	525.5	51.4	188	5	PCT-US95-04258-5	Sequence 5, Appli
3	370.5	36.2	114	3	US-08-722-126A-6	Sequence 6, Appli
4	370.5	36.2	114	5	PCT-US95-04258-6	Sequence 6, Appli
5	201	19.6	225	2	US-08-738-462-2	Sequence 6, Appli
6	201	19.6	225	5	PCT-US94-07587-2	Sequence 2, Appli
7	196.5	19.2	179	1	US-09-690-095-9	Sequence 9, Appli
8	196.5	19.2	179	2	US-08-650-578-2	Sequence 2, Appli
9	196.5	19.2	179	2	US-08-688-342-3	Sequence 3, Appli
10	196.5	19.2	179	2	US-08-113-789-3	Sequence 3, Appli
11	196.5	19.2	179	3	US-09-113-789-9	Sequence 9, Appli
12	196.5	19.2	199	5	PCT-US93-10418-4	Sequence 4, Appli
13	193	18.9	270	2	US-09-055-095-4	Sequence 4, Appli
14	193	18.9	270	2	US-08-809-494A-2	Sequence 2, Appli
15	193	18.9	270	4	US-09-352-302-2	Sequence 2, Appli
16	18.9	273	2	US-08-804-494A-4	Sequence 4, Appli	
17	193	18.9	273	4	US-09-352-302-4	Sequence 4, Appli
18	190	18.6	233	1	US-08-690-095-8	Sequence 8, Appli
19	190	18.6	233	3	US-09-113-789-8	Sequence 8, Appli
20	190	18.6	233	4	US-08-543-246B-2	Sequence 2, Appli
21	190	18.6	233	4	US-08-543-246B-21	Sequence 21, Appli
22	185.5	18.1	316	4	US-09-111-470-4	Sequence 4, Appli
23	184	18.0	215	1	US-08-690-095-7	Sequence 7, Appli
24	184	18.0	215	3	US-09-113-789-7	Sequence 7, Appli
25	184	18.0	215	4	US-08-543-246B-16	Sequence 16, Appli
26	184	18.0	215	4	US-08-543-246B-22	Sequence 22, Appli
27	17.8	231	3	US-09-113-789-6	Sequence 6, Appli	

ALIGNMENTS

Query Match	Score 525.5;	DB 3;	Length 188;
1	51.4%		

MS-08-650-578-2 MOLECULE TYPE: protein

Query Match 19.2%; Score 196.5; DB 2; Length 179;
 Best Local Similarity 32.7%; Pred. No. 1.4e-13; Indels 15; Gaps 7;
 Matches 53; Conservative 25; Mismatches 69; Indexes 15; Gaps 7;

Qy 35 CSQLVATLGLATLVLVLLVQWILCQGSN--YSTCACSPCPDRMKYGNHCYFSVE 92
 Db 20 CLSLMA-TLGILKNSFTKLSIEPAFTPGPNEILQKDSDCCSQCQEWKGYRCNCYFISSE 78

Qy 93 EKDWNSSLFCLARDSHLIVTDNQEMSLQVFLSEATCWIGL--RNNSGRWEDGSP 149
 Db 79 QKTWNESRHLCASQKSSLQQLQNTDLDLDEMS--SSQFYWIGLSYSEHTAWLWENGSA 136

Qy 150 NFSRISIISF---VOTGAINKNG-LQASCEVPLHGCKK 186
 Db 137 --SQLFPLSFETNTKNCIAYPNQNGNALDESCDKNRYICKQ 176

RESULT 9

US-08-688-342-3
 Sequence 3, Application US/08688342
 Patent No. 5871964

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice
 APPLICANT: Cocks, Benjamin G.
 APPLICANT: Goli, Surya K.
 APPLICANT: Hillman, Jennifer L.
 TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: US
 ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08-688,342
 FILING DATE: Filed Herewith

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0095-1 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 179 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1098616

US-08-688-342-3

Query Match 19.2%; Score 196.5; DB 2; Length 179;
 Best Local Similarity 32.7%; Pred. No. 1.4e-13; Indels 15; Gaps 7;
 Matches 53; Conservative 25; Mismatches 69; Indexes 15; Gaps 7;

Qy 35 CSQLVATLGLATLVLVLLVQWILCQGSN--YSTCACSPCPDRMKYGNHCYFSVE 92
 Db 20 CLSLMA-TLGILKNSFTKLSIEPAFTPGPNEILQKDSDCCSQCQEWKGYRCNCYFISSE 78

Qy 93 EKDWNSSLFCLARDSHLIVTDNQEMSLQVFLSEATCWIGL--RNNSGRWEDGSP 149
 Db 79 QKTWNESRHLCASQKSSLQQLQNTDLDLDEMS--SSQFYWIGLSYSEHTAWLWENGSA 136

Qy 150 NFSRISIISF---VOTGAINKNG-LQASCEVPLHGCKK 186
 Db 137 --SQLFPLSFETNTKNCIAYPNQNGNALDESCDKNRYICKQ 176

RESULT 10

US-09-113-788-3
 Sequence 3, Application US/09113788
 Patent No. 5969104

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice
 APPLICANT: Cocks, Benjamin G.
 APPLICANT: Goli, Surya K.
 APPLICANT: Hillman, Jennifer L.
 TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: US
 ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/113,788
 FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/688,342
 FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0095-1 CIP

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 179 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1098616

US-09-113-788-3

Query Match 19.2%; Score 196.5; DB 2; Length 179;
 Best Local Similarity 32.7%; Pred. No. 1.4e-13; Indels 15; Gaps 7;
 Matches 53; Conservative 25; Mismatches 69; Indexes 15; Gaps 7;

Qy 35 CSQLVATLGLATLVLVLLVQWILCQGSN--YSTCACSPCPDRMKYGNHCYFSVE 92
 Db 20 CLSLMA-TLGILKNSFTKLSIEPAFTPGPNEILQKDSDCCSQCQEWKGYRCNCYFISSE 78

Qy 93 EKDWNSSLFCLARDSHLIVTDNQEMSLQVFLSEATCWIGL--RNNSGRWEDGSP 149
 Db 79 QKTWNESRHLCASQKSSLQQLQNTDLDLDEMS--SSQFYWIGLSYSEHTAWLWENGSA 136

Qy 150 NFSRISIISF---VOTGAINKNG-LQASCEVPLHGCKK 186
 Db 137 --SQLFPLSFETNTKNCIAYPNQNGNALDESCDKNRYICKQ 176

RESULT 11
 US-09-113-789-9
 Sequence 9, Application US/09113789
 Patent No. 6034219
 GENERAL INFORMATION:
 APPLICANT: Hillman, Jennifer L.
 APPLICANT: Au-Young, Janice
 CITY: Palo Alto
 STATE: CA
 COUNTRY: U.S.
 ZIP: 94304
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/113-789
 FILING DATE:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/690, 095
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0110 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 179 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 IMMEDIATE SOURCE:
 LIBRARY: Genbank
 CLONE: 1098617
 ; US-09-113-789-9

Query Match 19 2%; Score 196 5; DB 3; Length 179;
 Best Local Similarity 32.7%; Pred. No. 1.4e-13; Indels 15; Gaps 7;
 Matches 53; Conservative 69; Mismatches 15; Gaps 7;
 Matches 53; Conservative 69; Indels 15; Gaps 7;
 QY 35 CSQLVAVITGLTAVLVLVILYQWILCGSN-YTCASCPSCPDRMKYGNHCYFSE 92
 DB 20 CLSIMA-TIGILKNSFTKISIEPAPFGPNIEQKDSDCSCQKWKVGRNCYCFISSE 78
 QY 93 EKDWNNSLEFLCLARDSHLLVTDNOEEMSLLQVFLSBAFCWIGL--RNNGWWRWDGSP 149
 DB 79 QKTRWESRHLICASQSSLLQLONTDEDFMS-SSQOFWIGLSEERFLWLNWNSAL 136
 QY 150 NFSRSSLNSNFS---VOTCGAINKG-LQASSECVLHGYCK 186
 DB 137 --SQLFPPSFETPNTKNCIAYNPNQNGNALDESCEDKRNICKQ 176
 RESULT 12
 PCT-US93-10418-4
 Sequence 4, Application PC/US9310418
 GENERAL INFORMATION:
 APPLICANT: Ziegler, Steven F.
 APPLICANT: Hjerrild, Kathryn A.
 TITLE OF INVENTION: Activation Antigen CD59
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Immunex Corporation
 STREET: 51 University Street
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98101
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/10418
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Sees, Kathryn A.
 REGISTRATION NUMBER: 32,172
 REFERENCE/DOCKET NUMBER: 2610-WO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 587-0430
 TELEFAX: (206) 233-0544
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 199 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US93/10418-4

Query Match 19 2%; Score 196 5; Length 199;
 Best Local Similarity 27.2%; Pred. No. 1.6e-13; Indels 33; Gaps 7;
 Matches 52; Conservative 27; Mismatches 79; Indels 33; Gaps 7;
 QY 17 QAQNDYGPQ-OKSSSSKPCSCSLVAITULGILAVLISVLQYQWILCGQSSNYSTCASC 73
 DB 18 RQQKDHGTSTHFEKIHSEG---STQSVIPWVLVWLVLITLILIALTALNQY---NCP 69
 QY 74 -SCPDRMKYGNHCYFSEVEEKDNSSLEFLCARDSHLWLNITDQEM 119
 DB 70 GLEYKLESSDHIVATCKNEWISYKRTCYFFTTKSWALQRSCEDAATLAVIDESEKDM 129
 QY 120 SLLQVFLSEAFCWIGLRN-NSGWRWEDGSLN-FSRISNSFVOTCGAANKNGQASS 175
 DB 130 TFLKRVSGELEHWIGLKEANQTWANGKFNFSWNLNTGG---RCVSVNHKNTAVD 185
 QY 176 GEPVLHGVCCK 186
 DB 186 CEFANFHWCNSK 196

RESULT 13
 US-09-055-095-4
 Sequence 4, Application US/09055095
 Patent No. 5945308
 GENERAL INFORMATION:
 APPLICANT: Tang, Y. Tom
 APPLICANT: Patterson, Chandra
 APPLICANT: Corley, Neil C.
 APPLICANT: Sather, Susan
 TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Dr.
 CITY: Palo Alto
 STATE: CA

ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
TELEFAX: 212 818-9479
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

Search completed: September 9, 2002, 15:00:04
Job time: 1123 sec

Job time: 1123 sec

OM protein - protein search, using sw model
Run on: September 9, 2002, 14:39:55 ; Search time 30.06 Seconds
Title: US-09-811-367B-1
Perfect score: 1023
Sequence: 1 MDSVIVKMLFLPTIQAN,..... GLOSSCEVPLHGVCKVRL 189
Scoring table: Blosum62
Gapop 10.0 , Gapext 0.5
Searched: 74574 seqs, 11073796 residues
Total number of hits satisfying chosen parameters: 74574
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS1/gcgdata/hold-geneseq/geneseq -emb1/AA2001 DAT: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match Length	DB ID	Description	
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2	1023	100.0	189	22	AAW11759 Human mast cell fu
3	789	77.1	843	22	ABG05451 Novel human diagno
4	548.5	53.6	188	22	AAE11760 Mouse mast cell fu
5	525.5	51.4	188	16	AAK77033 Mammalian mast cell
6	525.5	51.4	188	20	AAW88277 Rat mast cell func
7	525.5	51.4	188	22	AAE11761 Rat mast cell func
8	42.1	42.1	99	20	AAW88267 Human MAFa splice
9	370.5	36.2	114	16	AAR77472 Partial sequence o
10	30.0	30.0	70	20	AAW88266 Human MAFa splice
11	22.1	22.1	198	22	AAW88815 Human immune/haema

DT	XX	DE	Rat mast cell function-associated antigen (MAFA).
XX	OS	Rattus sp.	
FH		Location/Qualifiers	
FT	Key		
FT	Modified-site	82..84	
FT	/note=	"Asn is N-glycosylated"	
FT	Modified-site	97..99	/note= "Asn is N-glycosylated"
XX	W09854209-A2.		
XX	03-DEC-1998.		
XX	PF	29-MAY-1998;	98WO-GB01572.
XX	PR	31-MAY-1997;	97GB-0011148.
XX	PA	(PEPT-) PEPTIDE THERAPEUTICS LTD.	
XX	PT	Hewitt, EL, Lamers MBAC, Lamont A, Williams DH;	
XX	DR	WPI: 1999-059806/05.	
XX	DR	N-PSSD; AAV8A222.	
PS	PT	New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth	
XX	PT		
CC	CC	This is the amino acid sequence of rat mast cell function-associated antigen (MAFA), a type II membrane glycoprotein found on mast cells and basophils. The invention relates to cloning of the human MAFA molecule (see AAW88265), and to the discovery of splice variant (see AAW88265-67) of human MAFA that are not found in rat. Polypeptides and synthetic peptides (see AAW88258-64) based on human MAFA and human truncated MAFA, and polynucleotides encoding them, can be used in methods for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), and tumour growth.	
CC	CC		
XX	SQ	Sequence 188 AA:	
Query	Match	51.4%; Score 525.5; DB 20; Length 188;	
Best	Local Similarity	53.5%; Pred. No. 1.2e-46;	
Matches	100;	Conservative 29; Mismatches 57; Indels 1; Gaps 1.	
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Db	1	: : : : : : : :	60
Qy	61	COGSNYSTCASCPCSPDKWVKYGNHCVYFFVEEKWQNSLLEFLCARDSLQHSLVLTNDQEM	120
Db	61	: : : : : : : : :	120
Qy	121	LIQVFLSLPACFWIGLRLNNNGWRNBGSPLNFSRISNSNPFVOTCAINKNGLOASSCEVPL	180
Db	121	: : : : : : :	179
Qy	181	HGVCKV 187	
Db	180	: :	
Qy	180	qvicekv 186	

Db	180	qwickv 186
RESULT	8	
AAW88267	AAW88267	standard; Protein: 99 AA.
ID	AAW88267;	
AC	AAE11761;	
XX	AAE11761 standard; Protein: 188 AA.	
DE	Rat mast cell function associated antigen (MAFA) protein.	
XX	Rat; pharmaceutical composition; mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic.	
KW	Rat; pharmaceutical composition; mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic.	
OS	Rattus norvegicus.	
XX	Rattus norvegicus.	
PN	WO200170805-A2.	
XX	WO200170805-A2.	
PD	27-SEP-2001.	
XX	27-SEP-2001.	
PP	16-MAR-2001; 2001WO-US08596.	
XX	16-MAR-2001; 2001WO-US08596.	
PR	17-MAR-2000; 2000US-190716P.	
XX	17-MAR-2000; 2000US-190716P.	
PA	(GEMINI) GEMINI SCI INC.	
XX	(GEMINI) GEMINI SCI INC.	
PT	Takahashi N, Mikayama T;	
XX	Takahashi N, Mikayama T;	
DR	WPI; 2001-611482/70.	
DR	N-PSDB; AAD18736.	
XX	N-PSDB; AAD18736.	
PT	Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.	
XX	Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.	
EX	Example 1; Page 19; 49pp; English.	
CC	The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAFA) ligand on a target cell, and prevents or inhibits natural killer (NK)- or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is rat MAFA protein.	
SQ	Sequence 188 AA;	
Query Match	51.4%; Score 525.5; DB 22; Length 188;	
Best Local Similarity	53.5%; Pred. No. 1.2e-46;	
Matches	100; Conservative	
Indels	29; Mismatches	
Gaps	57; 1;	
Qy	MTDSVIYSMLEIPTATAQNDYGPQQKSSSSKSCSCLIVAITIGLTLTAVLVLVLYQWIL	
Db	MTDSVIYSMLEIPTATAQNDYGPQQKSSSSKSCSCLIVAITIGLTLTAVLVLVLYQWIL	
1	MTDSVIYSMLEIPTATAQNDYGPQQKSSSSKSCSCLIVAITIGLTLTAVLVLVLYQWIL	
madnslystleipaaprvqqdssrwkvihpcvsyvmlaqgltvilvmlsillyqrtl	madnslystleipaaprvqqdssrwkvihpcvsyvmlaqgltvilvmlsillyqrtl	60
Db	MTDSVIYSMLEIPTATAQNDYGPQQKSSSSKSCSCLIVAITIGLTLTAVLVLVLYQWIL	
1	MTDSVIYSMLEIPTATAQNDYGPQQKSSSSKSCSCLIVAITIGLTLTAVLVLVLYQWIL	
madnslystleipaaprvqqdssrwkvihpcvsyvmlaqgltvilvmlsillyqrtl	madnslystleipaaprvqqdssrwkvihpcvsyvmlaqgltvilvmlsillyqrtl	60
Qy	61 COGSNIVSTCASCPCPDRMKYGNHCYIFSVEEKDWNSLECLARDSHLLVTDNOENS	
Db	61 COGSNIVSTCASCPCPDRMKYGNHCYIFSVEEKDWNSLECLARDSHLLVTDNOENS	
1	61 COGSNIVSTCASCPCPDRMKYGNHCYIFSVEEKDWNSLECLARDSHLLVTDNOENS	
ccgskgfmcsqscprlpmrgshcyfsmekrdwnslkfadkgshllfpdqgnv	ccgskgfmcsqscprlpmrgshcyfsmekrdwnslkfadkgshllfpdqgnv	120
Db	61 COGSNIVSTCASCPCPDRMKYGNHCYIFSVEEKDWNSLECLARDSHLLVTDNOENS	
1	61 COGSNIVSTCASCPCPDRMKYGNHCYIFSVEEKDWNSLECLARDSHLLVTDNOENS	
ccgskgfmcsqscprlpmrgshcyfsmekrdwnslkfadkgshllfpdqgnv	ccgskgfmcsqscprlpmrgshcyfsmekrdwnslkfadkgshllfpdqgnv	120
Qy	121 LIQVFLSEAFCWIGLRRNNSGWRWEDEGSPLNFSRISSSFVQTCGAINKNGLQASSCVEPL	
Db	121 LIQVFLSEAFCWIGLRRNNSGWRWEDEGSPLNFSRISSSFVQTCGAINKNGLQASSCVEPL	
1	121 LIQVFLSEAFCWIGLRRNNSGWRWEDEGSPLNFSRISSSFVQTCGAINKNGLQASSCVEPL	
lfqeyygedfywiglrdidgwgweddpalisl-islnsvwqkogtihrglnhasceval	lfqeyygedfywiglrdidgwgweddpalisl-islnsvwqkogtihrglnhasceval	179
Qy	181 HGVCVKVRL 187	
Query Match	42.1%; Score 431; DB 20; Length 99;	
Best Local Similarity	50.3%; Pred. No. 3.5e-37;	
Matches	95; Conservative	
Indels	1;	
Gaps	90; 3;	
Qy	MTDSVIYSMLEIPTATAQNDYGPQQKSSSSKSCSCLIVAITIGLTLTAVLVLVLYQWIL	
Db	MTDSVIYSMLEIPTATAQNDYGPQQKSSSSKSCSCLIVAITIGLTLTAVLVLVLYQWIL	
1	MTDSVIYSMLEIPTATAQNDYGPQQKSSSSKSCSCLIVAITIGLTLTAVLVLVLYQWIL	
mtdslystleipaaprvqqdssrwkvihpcvsyvmlaqgltvilvmlsillyqrtl	mtdslystleipaaprvqqdssrwkvihpcvsyvmlaqgltvilvmlsillyqrtl	60
Qy	61 COGSNIVSTCASCPCPDRMKYGNHCYIFSVEEKDWNSLECLARDSHLLVTDNOENS	
Db	61 COGSNIVSTCASCPCPDRMKYGNHCYIFSVEEKDWNSLECLARDSHLLVTDNOENS	
1	61 COGSNIVSTCASCPCPDRMKYGNHCYIFSVEEKDWNSLECLARDSHLLVTDNOENS	
ccgskgfmcsqscprlpmrgshcyfsmekrdwnslkfadkgshllfpdqgnv	ccgskgfmcsqscprlpmrgshcyfsmekrdwnslkfadkgshllfpdqgnv	120
Db	61 COGSNIVSTCASCPCPDRMKYGNHCYIFSVEEKDWNSLECLARDSHLLVTDNOENS	
1	61 COGSNIVSTCASCPCPDRMKYGNHCYIFSVEEKDWNSLECLARDSHLLVTDNOENS	
ccgskgfmcsqscprlpmrgshcyfsmekrdwnslkfadkgshllfpdqgnv	ccgskgfmcsqscprlpmrgshcyfsmekrdwnslkfadkgshllfpdqgnv	120
Qy	121 LIQVFLSEAFCWIGLRRNNSGWRWEDEGSPLNFSRISSSFVQTCGAINKNGLQASSCVEPL	
Db	64 -----isssnfvqtcgaitknglnqasceval	
Qy	181 HGVCVKVRL 189	

OS	KW	cytostatic; gene therapy; vaccine; metastasis.
XX	XX	
PR	PR	Homo sapiens.
PR	PR	W020157182-A2.
XX	XX	
PD	09-AUG-2001.	
PR	17-JAN-2001;	2001W0-US01354.
PR	31-JAN-2000;	2000US-0179065.
PR	04-FEB-2000;	2000US-0180628.
PR	24-FEB-2000;	2000US-0184664.
PR	02-MAR-2000;	2000US-0186350.
PR	16-MAR-2000;	2000US-0189874.
PR	17-MAR-2000;	2000US-0190765.
PR	18-APR-2000;	2000US-0198123.
PR	19-MAY-2000;	2000US-0205515.
PR	07-JUN-2000;	2000US-0209457.
PR	28-JUN-2000;	2000US-0214886.
PR	07-JUL-2000;	2000US-0215135.
PR	07-JUL-2000;	2000US-0216647.
PR	11-JUL-2000;	2000US-0216880.
PR	11-JUL-2000;	2000US-0217487.
PR	14-JUL-2000;	2000US-0218290.
PR	26-JUL-2000;	2000US-0220963.
PR	14-AUG-2000;	2000US-0221647.
PR	14-AUG-2000;	2000US-0224118.
PR	14-AUG-2000;	2000US-0224513.
PR	14-AUG-2000;	2000US-0225214.
PR	14-AUG-2000;	2000US-0225266.
PR	14-AUG-2000;	2000US-0225267.
PR	14-AUG-2000;	2000US-0225668.
PR	14-AUG-2000;	2000US-0225720.
PR	14-AUG-2000;	2000US-0225947.
PR	14-AUG-2000;	2000US-0225758.
PR	14-AUG-2000;	2000US-0225759.
PR	18-AUG-2000;	2000US-0226279.
PR	14-AUG-2000;	2000US-0226681.
PR	22-AUG-2000;	2000US-0226868.
PR	01-SEP-2000;	2000US-0227182.
PR	01-SEP-2000;	2000US-0227009.
PR	30-AUG-2000;	2000US-0227924.
PR	01-SEP-2000;	2000US-0229287.
PR	01-SEP-2000;	2000US-0229343.
PR	01-SEP-2000;	2000US-0229344.
PR	05-SEP-2000;	2000US-0229345.
PR	05-SEP-2000;	2000US-0229509.
PR	06-SEP-2000;	2000US-0229513.
PR	06-SEP-2000;	2000US-0230437.
PR	06-SEP-2000;	2000US-0230438.
PR	08-SEP-2000;	2000US-0231242.
PR	08-SEP-2000;	2000US-0231243.
PR	12-SEP-2000;	2000US-0231968.
PR	14-SEP-2000;	2000US-0232397.
PR	14-SEP-2000;	2000US-0231413.
PR	08-SEP-2000;	2000US-0231414.
PR	14-SEP-2000;	2000US-0232080.
PR	08-SEP-2000;	2000US-0232081.
PR	14-SEP-2000;	2000US-0232398.
PR	14-SEP-2000;	2000US-0232399.
PR	21-SEP-2000;	2000US-0233065.
PR	14-SEP-2000;	2000US-02334223.
PR	21-SEP-2000;	2000US-02334240.
PR	25-SEP-2000;	2000US-02334997.
PR	05-JAN-2001;	2000US-0234997.

xx
 DE Peptide #645 encoded by human foetal liver single exon probe.
 xx
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.
 xx
 OS Homo sapiens.
 xx
 PN WO200157277-A2.
 xx
 PD 09-AUG-2001.
 xx
 PP 30-JAN-2001; 2001WO-US00669.
 xx
 PR 04-FEB-2000; 2000US-0180312.
 PR 26-MAY-2000; 2000US-020456.
 PR 30-JUN-2000; 2000US-0603408.
 PR 03-AUG-2000; 2000US-063366.
 PR 21-SEP-2000; 2000US-023687.
 PR 27-SEP-2000; 2000US-0236359.
 PR 04-OCT-2000; 2000GB-0024263.
 xx
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 xx
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 xx
 DR WPI; 2001-483447/52.
 xx
 PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human fetal liver -
 xx
 PS Claim 27: SEQ ID NO 25774; 639pp + sequence listing; English.
 xx
 CC The invention relates to a single exon nucleic acid probe for
 CC measuring human gene expression in a sample derived from human foetal
 CC liver. The single exon nucleic acid probes may be used for predicting,
 CC measuring and displaying gene expression in samples derived from human
 CC fetal liver. The present sequence is a peptide encoded by a single exon
 CC nucleic acid probe of the invention.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at [ftp.wipo.int/pub/published_pct_sequences](ftp://ftp.wipo.int/pub/published_pct_sequences).
 xx
 SQ Sequence 35 AA:
 Sequence 35 AA:

Query Match 21.2%; Score 217; DB 22; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.7e-15;
 Matches 35; Conservative 0; Mismatches 0; Index 0; Gaps 0;

QY 64 SNTSTCASCSPCPDRWMKIGNHCYFSVERKDWIS 98
 Db 1 snystcascpscpcdrwmkygnhcyfsveekdwis 35

Search completed: September 9, 2002, 14:59:44
 Job time: 1189 sec

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GenCore version 4.5

OM protein - protein search, using sw model
Run on: September 9, 2002, 14:59:46 ; Search time 27.34 seconds
(without alignments)
1195.905 Million cell updates/sec

Title: US-09-811-367B-1
Perfect score: 10:33

Sequence: 1 MTDIVIYSLMELPTATOQN. GLQASSEEVPLHGCKVYRL 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172944929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTRMBL19:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rickett:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_rvirus:
16: sp_bacteriap:
17: sp_archeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	%	Match Length	DB ID	Description	RESULT ID	RESULT	1
1	1023	100.0	189	4	043198	PRELIMINARY; PRT; 189 AA.	043198	043198	
2	1007	98.4	189	4	075613	DT 01-JUN-1998 (TREMBLrel. 05, Created) DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)	043198	043198	
3	994	97.2	195	4	096E93	DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
4	548.5	53.6	188	11	088713	DB MAST CELL FUNCTION-ASSOCIATED ANTIGEN;			
5	525.5	51.4	188	11	064335	GN MAFA.			
6	225	22.0	231	4	09NZS1	RA Eukaryota; Metacida; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.			
7	225	22.0	181	4	Q9DA03	RT "Human MAFA has alternatively spliced variants.";			
8	219.5	21.5	275	11	Q9DA03	RL Biochim Biophys Acta 1399:209-212(1998).			
9	210	20.5	227	11	09WU32	DR EMBL; AF034952; AAC34731.1;			
10	210	19.8	231	11	054872	DR HSSP; P06734; IHLI.			
11	203	19.7	233	6	Q95M15	DR InterPro; IPR01304; lectin_C.			
12	201.5	19.7	6	Q9MZK2	DR Pfam; PF00059; lectin_C; 1.				
13	201	19.6	225	22.1	Q9NZS1	DR SMART; SM00034; CLECT1.			
14	19.6	180	6	Q9MZK8	DR PROSITE; PS50041; C_TYPELECTIN_2; 1.				
15	19.5	19.5	231	6	Q9GK88	DR SEQUENCE; 189 AA; -21079 MW; 15E042A4OB2B4F6 CRC64;			
16	199.5	19.5	269	11	Q9d676	Qy Query Match 100.0%; Score 1023; DB 4; Length 189; Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

RT splicing of 5' exons in rhesus monkey decidua. ";

RL Immunogenetics 53:69-73(2001).

DR EMBL: AF294889; ARG34501.1; -.

DR ISSN: P06744; 1HIL.

DR InterPro: IPR001304; lectin_c.

DR SMART: SM0034; CLECT; 1.

DR PROSITE: PS50041; C_TYPELECTIN_2; 1.

SQ SEQUENCE: P231 AA: 26168 MW: D63C0F9126C41DB3 CRC64;

Query Match 19.5%; Score 199.5; DB 6; Length 231;

Best Local Similarity 28.3%; Pred. No 6.2e-14;

Matches 56; Conservative 33; Mismatches 92; Indels 17; Gaps 6;

Qy 2 TDSVIYSMLEPPTAQNDYGPQQ--KSSSKPSCSCLWATLGLITAVILSVLQW 59

Db 34 TPOEIF-QVELNUQNPESVHQIDQITDCQGLIPPERKLTAVLGLCIVLMAVTKVV 92

Qy 60 LC--QGSNYS-----TCASCPSCPDRMKYGNHCYVFSEVKDNSSLEFCLARDSHL 110

Db 93 LIPFPGEOSNSSLNTRQVKVRHGHCPHEWITVNSCIVIGERKRTWESLACTSKNSL 152

Qy 111 LVTIDQEMSLLQFVSEAFCWIGLRNNSG--WRWIDGSPLENFSRISNSSVOTGAIN 167

Db 153 LSIDNREMKFTAILPSS--WIGMFHNSSHHPWVTINGLTFKHEIKNSDNEAHNCAMLH 210

Qy 168 KNGLQASCEVPLHGVK 185

Db 211 ARGLKRNQCESTVYICK 228

Search completed: September 9, 2002, 15:03:39
 Job time: 233 sec